P. Paras

Re-run

RAW SEQUENCE LISTING DATE: 09/04/2003
PATENT APPLICATION: **US/09/804,409B** TIME: 09:36:14

Input Set : **N:\paola\US09804409B.raw.txt**
Output Set: **N:\CRF4\09032003\I804409B.raw**


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      2       KIEFFER, TIMOTHY J.
      3       CHEUNG, ANTHONY T.
      4 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
      5       EXPRESSION IN GUT
      6 <130> FILE REFERENCE: 029996/027 8721
C-->  7 <140> CURRENT APPLICATION NUMBER: US/09/804,409B
      8 <141> CURRENT FILING DATE: 2001-03-12
      9 <160> NUMBER OF SEQ ID NOS: 19
     10 <170> SOFTWARE: PatentIn Ver. 2.1
     12 <210> SEQ ID NO: 1
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     14 <212> TYPE: DNA
     15 <213> ORGANISM: Artificial Sequence
     16 <220> FEATURE:
     17 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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     22 <211> LENGTH: 22
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     24 <213> ORGANISM: Artificial Sequence
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     33 <213> ORGANISM: Artificial Sequence
     34 <220> FEATURE:
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     42 <213> ORGANISM: Artificial Sequence
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100       aaaaaattaa gcatctcacc ttttttgctc aaactaaaca gttttaaaac agttctgcct 1200
101       ggagtcatga tatgaaatac gatctatcat atttgcaatg ttctgttcaa ttgtggctgc 1260
102       accaggaaat gagaagctat ttctttatag gcacaaataa aaagatagtc attatctgta 1320
103       aaattcttat gacatggcag caagcccaag aaacctttct aaacaaggcg tgaaaacgca 1380
104       gagatgtcct tgcaattagt catgtctatc tgacagattt cttcctttct aagggaattt 1440
105       gtgctgaaca ttttatttcg agcctcagag ataaaagaag ggggaagaag ctgtagtttt 1500
106       tgctacataa gacaggtggc gtaagcatgc aacgctttaa aaaaatatct aaagtgattg 1560
107       ttttctctcg gattctttga aaaagctcgc ctgcgctggg gtttgaggct gagccggtga 1620
108       cgtcagcgtg gaatgcggag tcaggcgccc aggctctcta taagccgagg agctgtccgg 1680
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113 <211> LENGTH: 2623
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115 <213> ORGANISM: Mus musculus
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118       ccccttcact ggggtgtacc agtttaccct ggactgtcta agcaacaaga aggatagaca 120
119       tggcctacca cagatttcat gtctgccact ggctatgtca gaacatgtag gagcttttgg 180
120       aatcagtgaa acaggtattt tcagactgcc ttccctgcgt ggggctttcc cgaagccata 240
121       tttttcctag agtcagcctt tcccagctga ggacaagctg tactggacag atgccagcca 300
122       cttgaactgg gaatacatgg tcatttaggc agctggctta tctcatccat ggtacttgat 360
123       ggcttcgggt cagcacctca cagaaagttc agacgggagg cttccgagaa aacagagaag 420
124       caggcaggag atcctgcagg caatcctcct gctccacagc ctgcatggac ttccctcagc 480
125       cttagtgcgt gtgggtccca tctgagaaca ttggttatat gttattttca aaccgatctg 540
126       cctttaagga gtggaagaaa aaaactgtgg tgtttgggct acctttatga taatggcctt 600
127       ttcatcctcc taataaatat tgccaagtag ggtagattct atacgaaagc tcttaaccca 660
128       tggtattagc aaatcatgta ggtgctaata atgaatactg gatgcagtca gtacagggat 720
129       ataaaatgga atgtaagagc ctgttgctat gaatggttag ctaactagat gttgtacaag 780
130       aaatgttgac gttatgacgt gtggaaactt ggtattgaag atgtggactc gaaactttgt 840
131       ggatttttg atgccatgat aaaaatgtga agaatactgt tccttaccaa aaagaagaag 900
132       aagaaggaga aggaggagga agaggaggag gaggaagaag agggggagga agaagaagag 960
133       aaggaggagg aagaggagga ggaggaagaa gaggaggagg aggaagaaga agagaaggag 1020
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135       ggggtgccat cagaatacca gatactccag acatagtcac agaaggactg gtttgtttgt 1140
136       taaataggtg ctttgaaaag tttgtgggga aacctgcagt gagattgtgt gtcttagaaa 1200
137       tgataggcaa gattcatcca caagaatgcg acaagatggc tgcctgaaca agccctgaac 1260
138       attaacagca ccagtagacc tgcttacacg gaagaaagca atctcatagg ccctcacccc 1320
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142       gaaaaggccc catgttagag agggagcaag gtgggcatgg aggtatggaa ggagttggaa 1560
143       ggaggggtga gaaggggaaa gtgatgtaat tatcttttaa tttataaaaa aataaaaaat 1620
144       gggctggtga gatggctcag tgggtaagag cacccgactg cttcttccga aggtctggag 1680
145       ttcaaatccc agcaaccaca tggtggctca caaccatccg taacgagatc tggcgccctc 1740
146       ttctggagtg tctgaagaca gctacagtgt acttacatat aataaataaa taaatctttt 1800
147       aaaaaaaata aaaaataaaa tattagaata aaatgtagag gaatattttt aatttaacaa 1860
148       cttgggtgtg gcaaaagctt tcttcaacaa aaacttaatc cctcagataa gaaaagacta 1920
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150        cttgagcaga acttgagttg taacttgttg ggaaacacaa cacccttggc aaacaaaaga 2040
151        ttactagata ttttagatga aatataaaaa tactttccac aactgatagg taggaaacag 2100
152        ttcaatagta atataattat tgaacaaata atccttaaaa gaagaaatcc agaggaatag 2160
153        caagttaggg gaagagaggg tgtgtgtgtg tgtgtgtgcg cgcacattta tagccaaaat 2220
154        agatgatata cttaaatgaa catgccatta aaacccatta ttttgcatac agtttacata 2280
155        tgctaatgaa tacttaaaaa aaaaacattg ggattggaga gaaatggctc agtggttaag 2340
156        agttcaattc ccagcaacca catgattgct cacaaccatc tgtaatggga tctgatgcct 2400
157        tcttctggta tgtctgaaga aagtgaccgt gtacttataa ttataaataa ataaatcttt 2460
158        aaccaaaaaa cccccataat ttcaacaaca gatatgtcct ggtctgaggc ttccaggcat 2520
159        agaaatagaa acacacagag tgtggagcca gtgcggttca ggtccgccat tccagttcag 2580
160        gcttcagacc aagagaaagg gaaaagaaga gacaagcaac aag                    2623
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163 <211> LENGTH: 226
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 8
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168        cccgggaacg gcggcgggcg gggcgggagg cggggcccgg cccgttaaga agagcgtggc 120
169        cggccgcggc caccgctggc cccagggaaa gccgagcggc caccgagccg gcagagaccc 180
170        accgagcggc ggcggaggga gcgacgccgg ggcgcacgag ggcacc                 226
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173 <211> LENGTH: 110
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 9
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179        Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
180                     20                  25                  30
181        Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
182                 35                  40                  45
183        Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
184             50                  55                  60
185        Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
186         65                  70                  75                  80
187        Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
188                         85                  90                  95
189        Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
190                    100                 105                 110
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194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
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198        gcctcctgcc cctgctggcg ctgctggccc tctgggacc tgacccagcc gcagcctttg 120
199        tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac 180
200        gaggcttctt ctacacaccc aagacccgcc gggaggcaga ggacctgcag gtggggcagg 240
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203       agaactactg caactagacg cagcccgcag gcagcccccc acccgccgcc tcctgcaccg 420
204       agagagatgg aataaagccc ttgaaccagc                                  450
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208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 11
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213       Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
214                    20                  25                  30
215       Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
216                35                  40                  45
217       Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
218            50                  55                  60
219       Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
220        65                  70                  75                  80
221       Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
222                        85                  90                  95
223       Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
224                   100                 105                 110
225       Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
226               115                 120                 125
227       Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
228           130                 135                 140
229       Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
230       145                 150                 155                 160
231       Leu Asp Leu Ser Pro Gly Cys
232                       165
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235 <211> LENGTH: 3408
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238 <400> SEQUENCE: 12
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241       caagatgaca ccaaaaccct catcaagaca attgtcacca ggatcaatga catttcacac 180
242       acgcagtcag tctcctccaa acagaaagtc accggtttgg acttcattcc tgggctccac 240
243       cccatcctga ccttatccaa gatggaccag acactggcag tctaccaaca gatcctcacc 300
244       agtatgcctt ccagaaacgt gatccaaata tccaacgacc tggagaacct ccgggatctt 360
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247       agcaggctgc aggggtctct gcaggacatg ctgtggcagc tggacctcag ccctgggtgc 540
248       tgaggccttg aaggtcactc ttcctgcaag gactacgtta agggaaggaa ctctggcttc 600
249       caggtatctc caggattgaa gagcattgca tggacacccc ttatccagga ctctgtcaat 660
250       ttccctgact cctctaagcc actcttccaa aggcataaga ccctaagcct ccttttgctt 720
251       gaaaccaaag atatatacac aggatcctat tctcaccagg aaggggqtcc acccagcaaa 780
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L:7 M:270 C: Current Application Number differs, Wrong Format